

Report

	assembly
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	2883895
Total length (>= 5000 bp)	2883895
Total length (>= 10000 bp)	2883895
Total length (>= 25000 bp)	2883895
Total length (>= 50000 bp)	2848149
# contigs	2
Largest contig	2848149
Total length	2883895
Reference length	2845392
GC (%)	37.49
Reference GC (%)	37.52
N50	2848149
NG50	2848149
N75	2848149
NG75	2848149
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2848149
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	1685
Genome fraction (%)	100.000
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.85
# indels per 100 kbp	54.58
Largest alignment	2160111
Total aligned length	2882210
NA50	2160111
NGA50	2160111
NA75	686353
NGA75	2160111
LA50	1
LGA50	1
LA75	2
LGA75	1

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

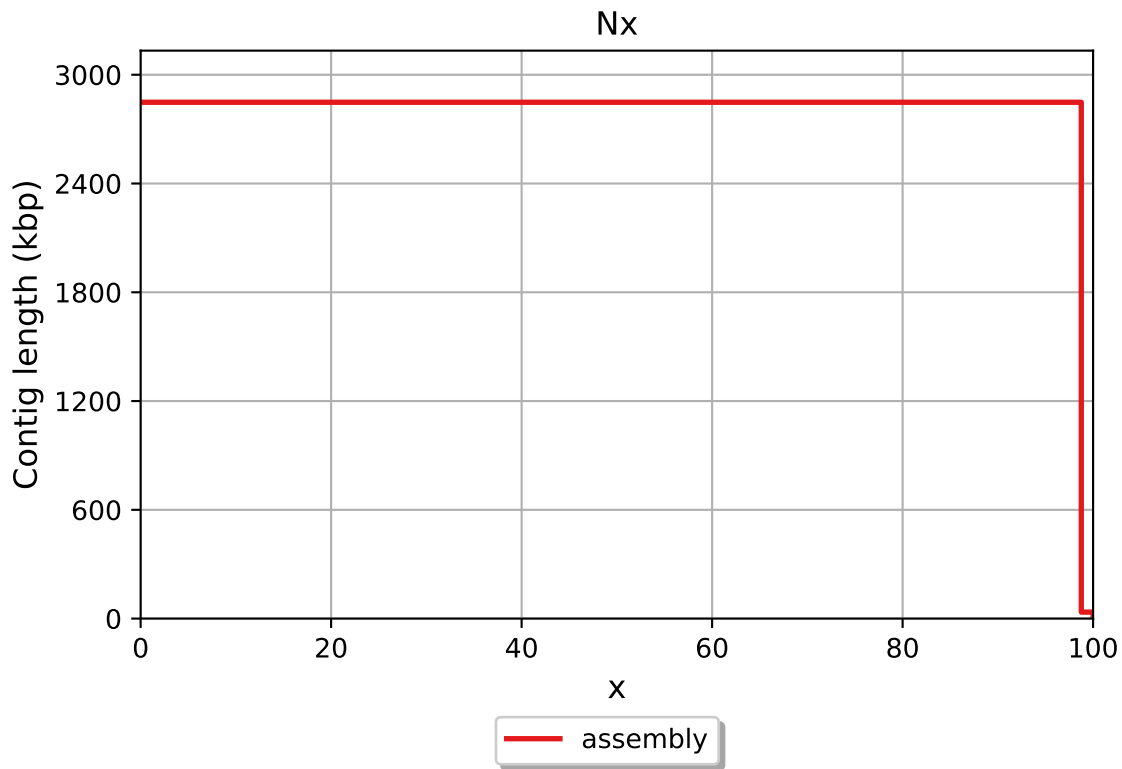
	assembly
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2848149
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	394
# indels	1553
# indels (<= 5 bp)	1550
# indels (> 5 bp)	3
Indels length	1756

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

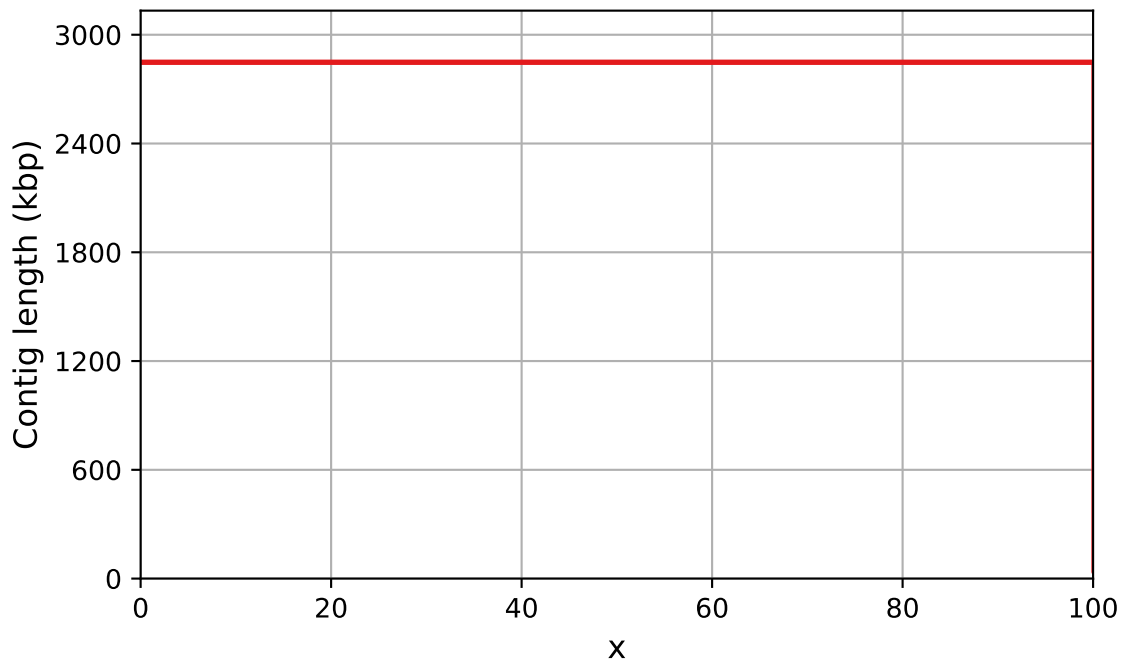
Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	1685
# N's	0

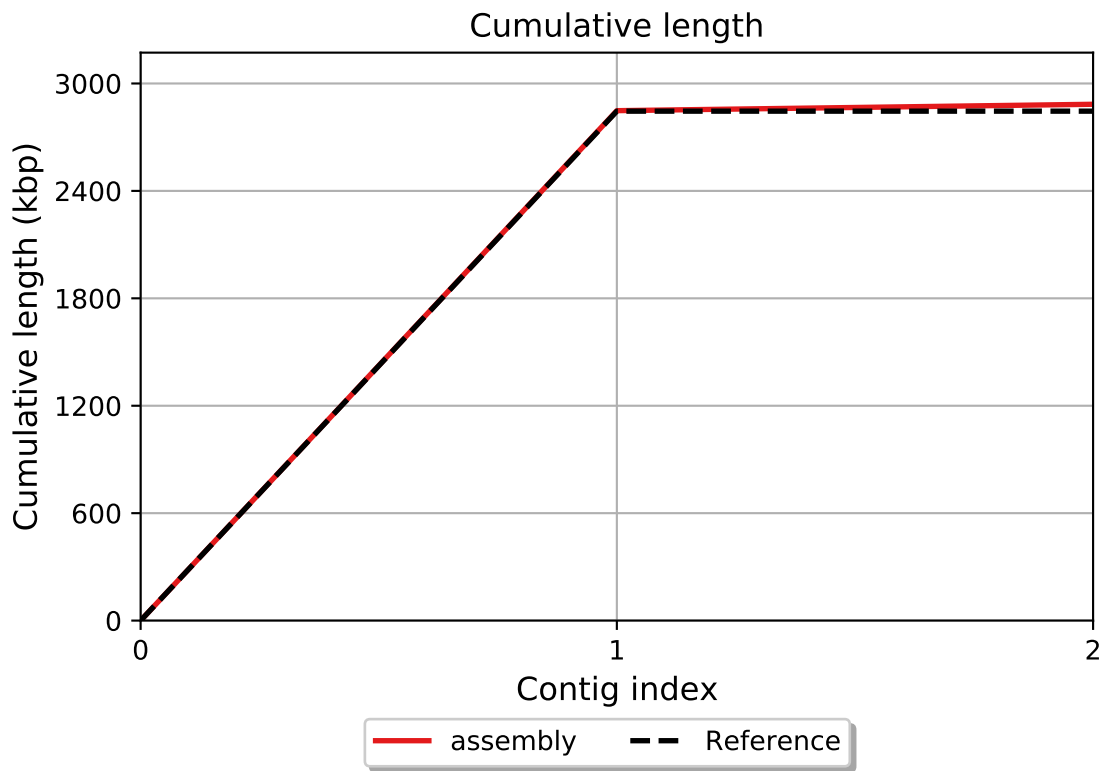
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



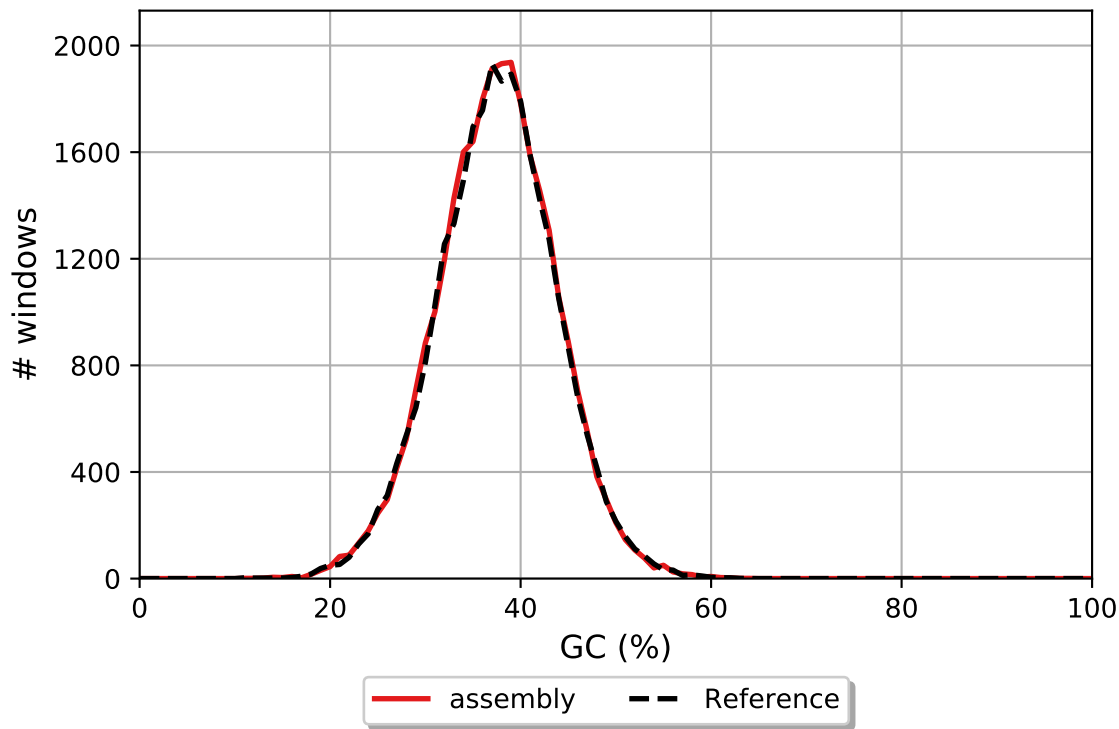
NGx



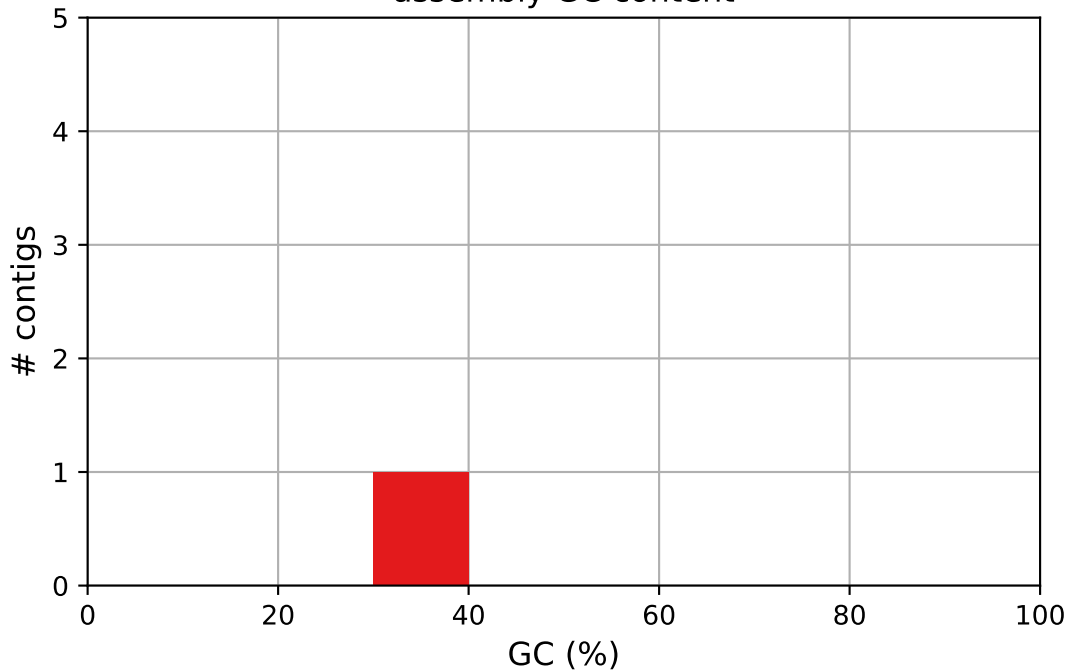
— assembly



GC content

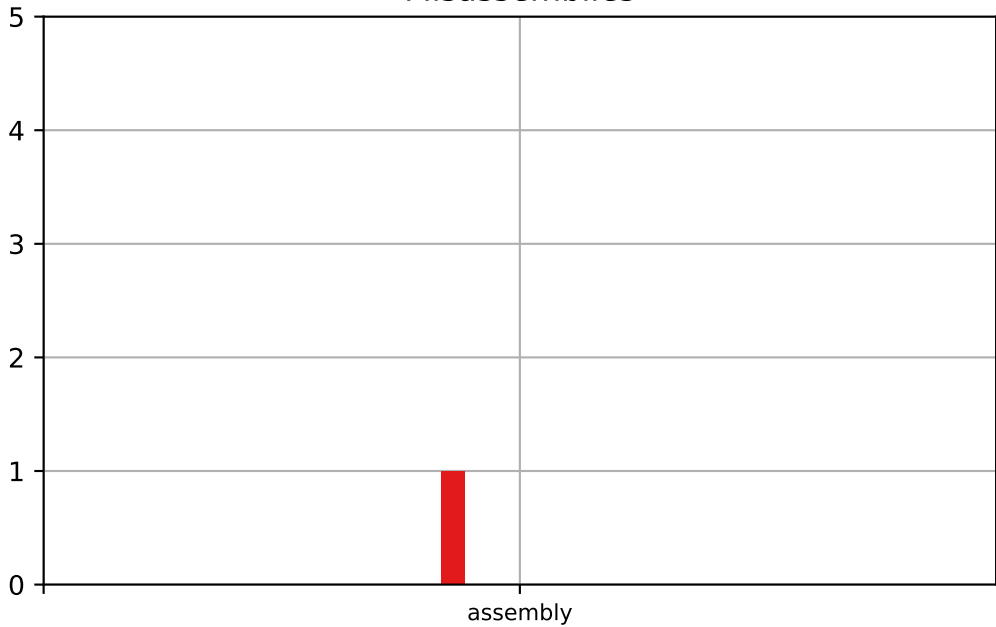


assembly GC content

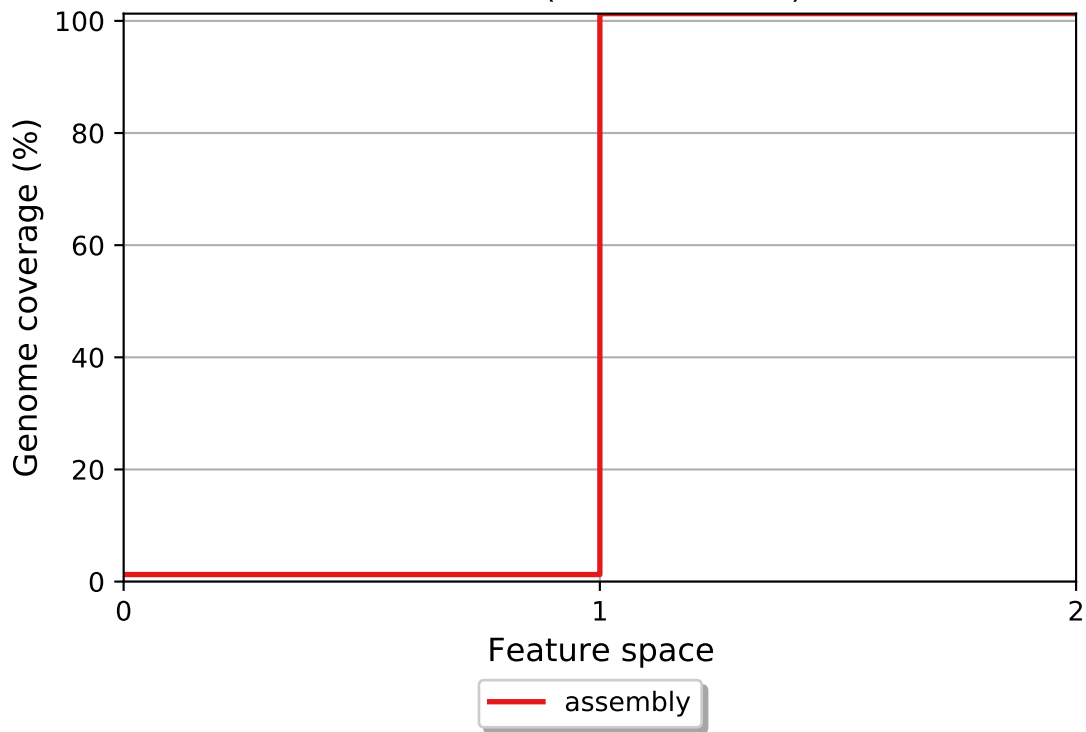


assembly

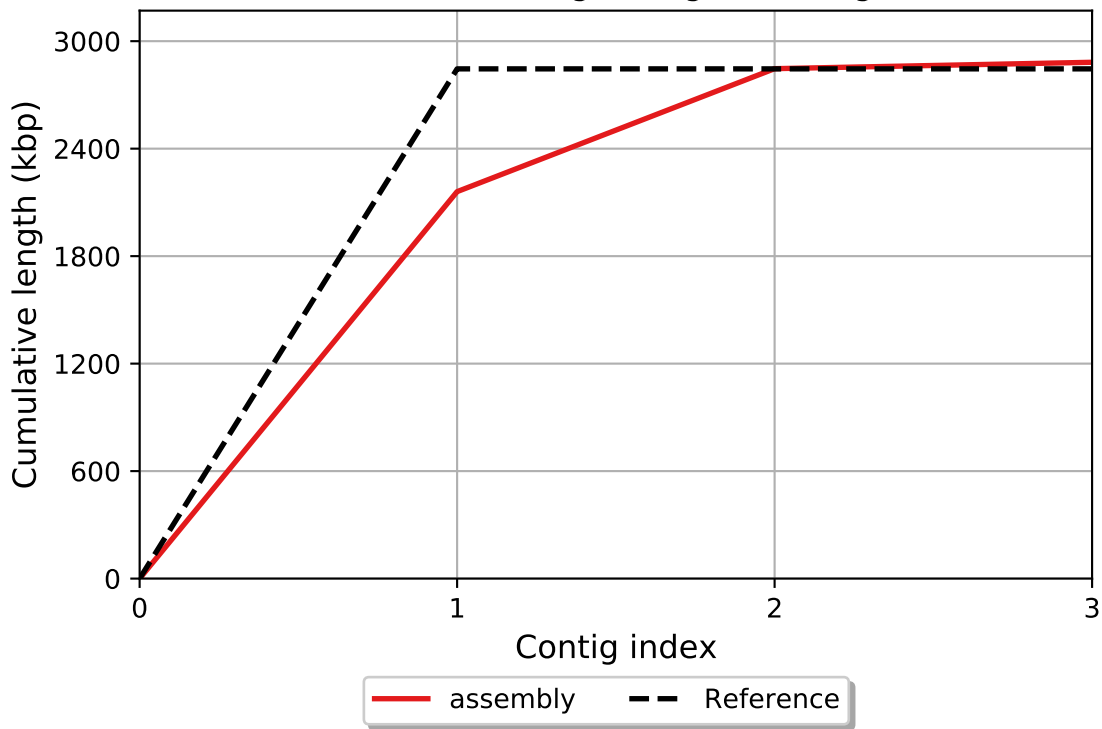
Misassemblies



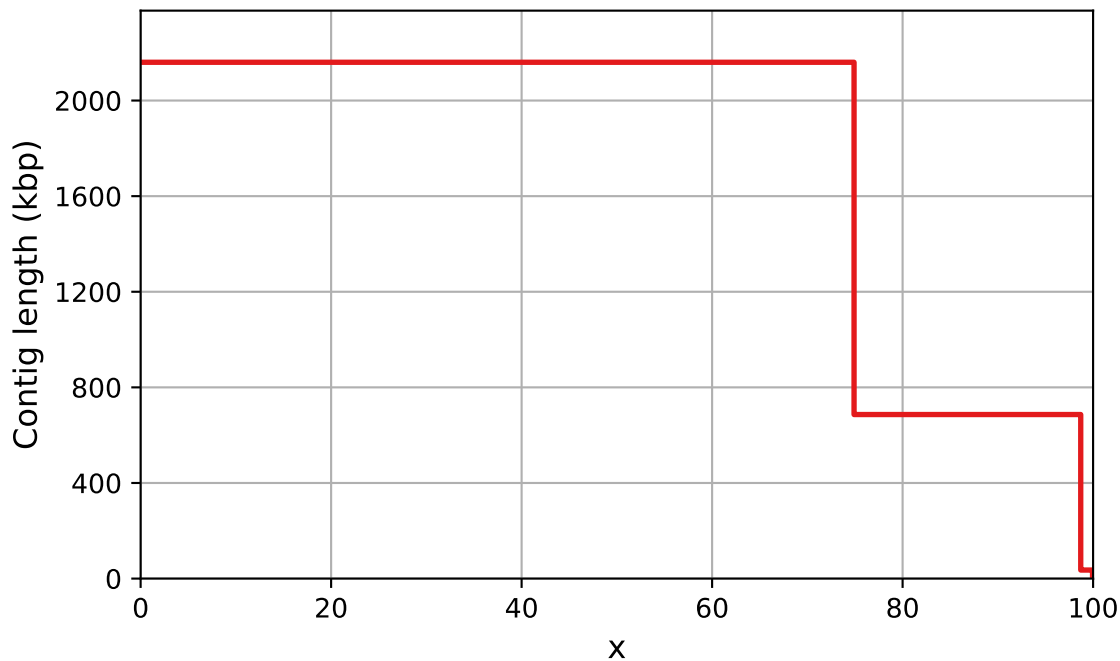
FRCurve (misassemblies)



Cumulative length (aligned contigs)

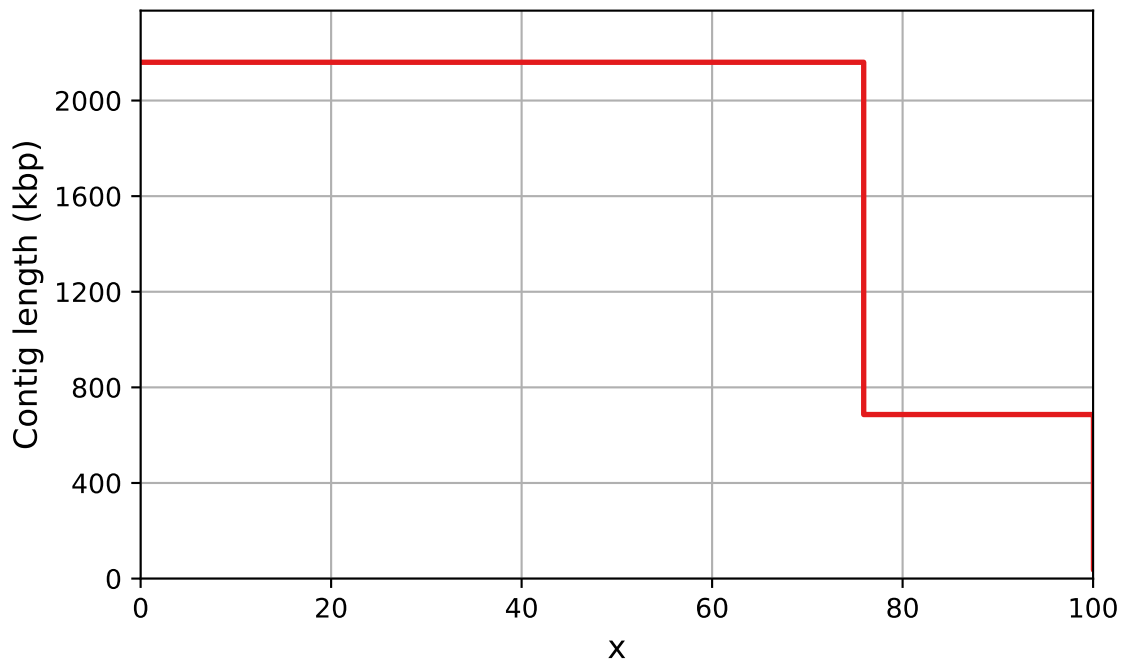


NAx



— assembly

NGAx



— assembly